GAP of: NvEcR10prtnseqwhole.txt   check: 4332   from: 1   to: 444

  to: MpEcR   check: 9113   from: 1   to: 450

  Symbol comparison table:
/usr/local/gcg/gcgcore/data/rundata/blosum62.cmp
  CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
          substitution matrices from protein blocks. Proc. Natl.
Acad.
          Sci. USA 89: 10915-10919.

          Gap Weight: 8   Average Match: 2.912
       Length Weight: 2   Average Mismatch: -2.003

          Quality: 1518   Length: 474   N viridula EcR (1)
            Ratio: 3.419   Gaps: 6   vs M pusicae EcR
  Percent Similarity: 79.762   Percent Identity: 72.857

        Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =   2
                    . =   1

GAP of: NvEcR11prtnseqwhole.txt   check: 6564   from: 1   to: 464

  to: MpEcR   check: 9113   from: 1   to: 450

  Symbol comparison table:
/usr/local/gcg/gcgcore/data/rundata/blosum62.cmp
  CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
          substitution matrices from protein blocks. Proc. Natl.
Acad.
          Sci. USA 89: 10915-10919.

          Gap Weight: 8   Average Match: 2.912
       Length Weight: 2   Average Mismatch: -2.003

          Quality: 1510   Length: 496   N viridula (2)
            Ratio: 3.356   Gaps: 7   vs M pusicae EcR
  Percent Similarity: 80.144   Percent Identity: 73.445

GAP of: MpEcR   check: 9113   from: 1   to: 450

  to: BtEcR   check: 8626   from: 1   to: 416

Symbol comparison table:
/usr/local/gcg/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
        substitution matrices from protein blocks. Proc. Natl.
Acad.
        Sci. USA 89: 10915-10919.

           Gap Weight: 8   Average Match: 2.912
        Length Weight: 2   Average Mismatch: -2.003

              Quality: 1450   Length: 451   M pussione EcR
                Ratio: 3.486   Gaps: 6   vs B tabaci EcR
   Percent Similarity: 78.554   Percent Identity: 71.566